
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=22; hr=9; min=26; sec=4; ms=670;]

Reviewer Comments:

<110> The University of Newcastle

Connolly, Bernard

Fogg, Mark

Pearl, Laurence

<120> DNA POLYMERASES

<130> P89103PWO

<140> 10511130

<141> 2005-08-15

<150> PCT/GB2003/001623

<151> 2003-04-15

<160> 32

Numeric identifier <160> must reflect the total number of sequences found in the sequence listing. This file contains 33 SEQ ID numbers, but <160> states there are 32. Please make all necessary changes.

<210> 13

<211> 103

<212> PRT

<213> RB69

* * * * * * * * *

Numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." Please make all necessary changes.

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<210> 33
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<211> 13

<212> PRT

<213> Unknown

<220>

<223> amino acid motif where X can be any amino acid

<400> 33

Glu Xaa Xaa Ile Xaa Phe/Tyr Xaa Xaa Xaa Tyr Xaa Xaa Asp 1 5 10

Numeric identifier <211> must reflect the total number of amino acids in the sequence. <211> states there are 13 amino acids in SEQ ID # 33, but the actual count is 14. Please make all necessary changes.

A sequence cannot contain any non-sequence related symbols. Please remove "/" from SEQ ID # 33.

Validated By CRFValidator v 1.0.3

Application No: 10511130 Version No: 2.0

Input Set:

Output Set:

Started: 2008-09-20 06:22:41.144 **Finished:** 2008-09-20 06:22:44.841

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 697 ms

Total Warnings: 23
Total Errors: 2

No. of SeqIDs Defined: 32
Actual SeqID Count: 33

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Input Set:

Output Set:

Started: 2008-09-20 06:22:41.144 **Finished:** 2008-09-20 06:22:44.841

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 697 ms

Total Warnings: 23

Total Errors: 2

No. of SeqIDs Defined: 32

Actual SeqID Count: 33

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E	330	Invalid protein , found in SEQID(33) POS (6) Invalid
W	333	tabs used in amino acid numbering SEQID (33)
E	252	Calc# of Seq. differs from actual; 32 seqIds defined; count=33

SEQUENCE LISTING

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15

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Arg	Thr	Phe 35	Arg	Pro	Tyr	Ile	Tyr 40	Ala	Leu	Leu	Arg	Asp 45	Asp	Ser	Lys
Ile	Glu 50	Glu	Val	Lys	Lys	Ile 55	Thr	Gly	Glu	Arg	His 60	Gly	Lys	Ile	Val
Arg 65	Ile	Val	Asp	Val	Glu 70	Lys	Val	Glu	Lys	Lys 75	Phe	Leu	Gly	Lys	Pro 80
Ile	Thr	Val	Trp	Lys 85	Leu	Tyr	Leu	Glu	His 90	Pro	Gln	Asp	Val	Pro 95	Thr
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Thr 145	Leu	Tyr	His	Glu	Gly 150	Glu	Glu	Phe	Gly	Lys 155	Gly	Pro	Ile	Ile	Met 160
Ile	Ser	Tyr	Ala	Asp 165	Glu	Asn	Glu	Ala	Lys 170	Val	Ile	Thr	Trp	Lys 175	Asn
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Thr	Tyr 210	Asn	Gly	Asp	Ser	Phe 215	Asp	Phe	Pro	Tyr	Leu 220	Ala	Lys	Arg	Ala
Glu 225	Lys	Leu	Gly	Ile	Lys 230	Leu	Thr	Ile	Gly	Arg 235	Asp	Gly	Ser	Glu	Pro 240

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Glu	Lys 290	Val	Tyr	Ala	Asp	Glu 295	Ile	Ala	Lys	Ala	Trp 300	Glu	Ser	Gly	Glu
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Tyr	Glu	Leu	Gly	Lys 325	Glu	Phe	Leu	Pro	Met 330	Glu	Ile	Gln	Leu	Ser 335	Arg
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Ala	Pro 370	Asn	Lys	Pro	Ser	Glu 375	Glu	Glu	Tyr	Gln	Arg 380	Arg	Leu	Arg	Glu
Ser 385	Tyr	Thr	Gly	Gly	Phe 390	Val	Lys	Glu	Pro	Glu 395	Lys	Gly	Leu	Trp	Glu 400
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Thr	His	Asn	Val 420	Ser	Pro	Asp	Thr	Leu 425	Asn	Leu	Glu	Gly	Cys 430	Lys	Asn
Tyr	Asp	Ile 435	Ala	Pro	Gln	Val	Gly 440	His	Lys	Phe	Суз	Lys 445	Asp	Ile	Pro
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Lys Ly:	595					600				_	605			
Gly Let)				615					620		-		
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Ala Vai			645					650	_				655	
Ile Pro		660					665					670		
His Glu	1 Tyr 675	Lys	Ala	Ile	Gly	Pro 680	His	Val	Ala	Val	Ala 685	Lys	TÀS	Leu

Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile

700 695 690

Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu 705 710 715 720

Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu 725 730 735

Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr 740 745 750

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<210> 2

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<212> PRT

<213> Pyrococcus furiosus

<400> 2

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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg 50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile 65 70 75

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85

90

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Ser Tyr Ala	Asp Glu 165	Asn Glu	Ala	Lys	Val 170	Ile	Thr	Trp	Lys	Asn 175	Ile
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Lys Leu Gly 225	Ile Lys	Leu Thr 230	Ile	Gly	Arg	Asp 235	Gly	Ser	Glu	Pro	Lys 240
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His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Leu	Glu	Gly	Суз	Lys 430	Asn	Tyr	
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				725					730	Glu				735	
			740					745		Glu			750	_	-
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Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys 35 40 45

Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val 50 60

Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro 65 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr

85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu \$100\$ 105 110

Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile 115 120 125

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Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met 145 150 155 160

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Lys	Met	Gln	Arg	Ile 245	Gly	Asp	Met	Thr	Ala 250	Val	Glu	Val	Lys	Gly 255	Arg
Ile	His	Phe	Asp 260	Leu	Tyr	His	Val	Ile 265	Thr	Arg	Thr	Ile	Asn 270	Leu	Pro
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370 375 380

Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu 385 390 395 400

Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile 405 410 415

Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn 420 425 430

Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro 435 440 445

Gly Phe Ile Pro Ser Leu Leu Gly His Leu L